



# Sequence Listing

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<120> NOVEL COMPOSITIONS AND METHODS FOR THE TREATMENT OF  
IMMUNE RELATED DISEASES

<130> P1974R1-US

<140> US 10/658,482

<141> 2003-09-09

<150> US 60/410,062

<151> 2002-09-11

<160> 9

<210> 1

<211> 831

<212> DNA

<213> Homo sapiens

<400> 1

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tgggcccagg ggctgaggca ggctccctc gcctcaggaa tgatgacagg 150  
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gggctctgtg gagagcagcg gggagaggac tgtgccgagc tgcattgacta 750  
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<210> 2  
 <211> 244  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Met Arg Trp Cys Leu Leu Leu Ile Trp Ala Gln Gly Leu Arg Gln  
 1 5 10 15  
 Ala Pro Leu Ala Ser Gly Met Met Thr Gly Thr Ile Glu Thr Thr  
 20 25 30  
 Gly Asn Ile Ser Ala Glu Lys Gly Gly Ser Ile Ile Leu Gln Cys  
 35 40 45  
 His Leu Ser Ser Thr Thr Ala Gln Val Thr Gln Val Asn Trp Glu  
 50 55 60  
 Gln Gln Asp Gln Leu Leu Ala Ile Cys Asn Ala Asp Leu Gly Trp  
 65 70 75  
 His Ile Ser Pro Ser Phe Lys Asp Arg Val Ala Pro Gly Pro Gly  
 80 85 90  
 Leu Gly Leu Thr Leu Gln Ser Leu Thr Val Asn Asp Thr Gly Glu  
 95 100 105  
 Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr Tyr Thr Gly  
 110 115 120  
 Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu His Gly  
 125 130 135  
 Ala Arg Phe Gln Ile Pro Leu Leu Gly Ala Met Ala Ala Thr Leu  
 140 145 150  
 Val Val Ile Cys Thr Ala Val Ile Val Val Val Ala Leu Thr Arg  
 155 160 165  
 Lys Lys Lys Ala Leu Arg Ile His Ser Val Glu Gly Asp Leu Arg  
 170 175 180  
 Arg Lys Ser Ala Gly Gln Glu Glu Trp Ser Pro Ser Ala Pro Ser  
 185 190 195  
 Pro Pro Gly Ser Cys Val Gln Ala Glu Ala Ala Pro Ala Gly Leu  
 200 205 210  
 Cys Gly Glu Gln Arg Gly Glu Asp Cys Ala Glu Leu His Asp Tyr  
 215 220 225  
 Phe Asn Val Leu Ser Tyr Arg Ser Leu Gly Asn Cys Ser Phe Phe  
 230 235 240  
 Thr Glu Thr Gly

<210> 3  
 <211> 1006  
 <212> DNA

<213> Homo sapiens

<400> 3

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tgactatgct gaccacagc aatactttaa tgtcctgagc tacagaagcc 750
tagagagctt cattgctgta tcgaagactg gctaacgaca gctctctatc 800
cctctcccta tgtctctctc tctgtctctc tctgtctctc tctgtctctg 850
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tgtgtgtatg tgtgtataca tcattaatgt tcattaacac taactgcata 950
tgggtggagga ccaggaaata aaagtttgtg ttgctaataa aattaagtgc 1000
taactt 1006
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<210> 4

<211> 241

<212> PRT

<213> Homo sapiens

<400> 4

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Met His Gly Trp Leu Leu Val Trp Val Gln Gly Leu Ile Gln
 1          5          10          15

Ala Ala Phe Leu Ala Thr Gly Ala Thr Ala Gly Thr Ile Asp Thr
          20          25          30

Lys Arg Asn Ile Ser Ala Glu Glu Gly Gly Ser Val Ile Leu Gln
          35          40          45

Cys His Phe Ser Ser Asp Thr Ala Glu Val Thr Gln Val Asp Trp
```

	50	55	60
Lys Gln Gln Asp Gln Leu Leu Ala Ile Tyr Ser Val Asp Leu Gly	65	70	75
Trp His Val Ala Ser Val Phe Ser Asp Arg Val Val Pro Gly Pro	80	85	90
Ser Leu Gly Leu Thr Phe Gln Ser Leu Thr Met Asn Asp Thr Gly	95	100	105
Glu Tyr Phe Cys Thr Tyr His Thr Tyr Pro Gly Gly Ile Tyr Lys	110	115	120
Gly Arg Ile Phe Leu Lys Val Gln Glu Ser Ser Val Ala Gln Phe	125	130	135
Gln Thr Ala Pro Leu Gly Gly Thr Met Ala Ala Val Leu Gly Leu	140	145	150
Ile Cys Leu Met Val Thr Gly Val Thr Val Leu Ala Arg Lys Lys	155	160	165
Ser Ile Arg Met His Ser Ile Glu Ser Gly Leu Gly Arg Thr Glu	170	175	180
Ala Glu Pro Gln Glu Trp Asn Leu Arg Ser Leu Ser Ser Pro Gly	185	190	195
Ser Pro Val Gln Thr Gln Thr Ala Pro Ala Gly Pro Cys Gly Glu	200	205	210
Gln Ala Glu Asp Asp Tyr Ala Asp Pro Gln Glu Tyr Phe Asn Val	215	220	225
Leu Ser Tyr Arg Ser Leu Glu Ser Phe Ile Ala Val Ser Lys Thr	230	235	240

Gly

```

<210> 5
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide probe - forward primer

<400> 5
cgtcctatct gcagtcggct actttca 27

<210> 6
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide probe - reverse primer

<400> 6

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ccagaagatg cctctggttg ctaacca 27

<210> 7

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide probe - forward primer

<400> 7

caggaccagc ttctggccat ttatagtgt 29

<210> 8

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide probe - reverse primer

<400> 8

ctgcttccag tcgacttggg tcactt 26

<210> 9

<211> 46

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide probe

<400> 9

cctggtggga ttacaaggg gagaatattc ctgaaggtcc aagaaa 46